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B

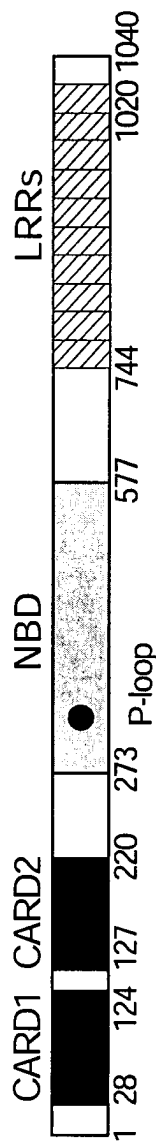


Figure 1

# A

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Nod2(2)	127	SEHP-ARDLOSHPAVERHSHAV	--ENMIDLAERGEVSQ	ECDEIRLPIT	PSQARRLLDVAWVKWACOKLIAACE	ACADSOSP	KLGGMD
Nod1	15	ESPHIQILKSNRELLVTHIENTQ	--CLVDNLLKNDYFSD	EDAEIVACPTQ	--PDKVRKILDLVOSKEEVS	SEFLYLQO	--LADAVDLISWILLE
RICK	434	-GTAQQTOSKREDIVNCTEAC	--NOSLDALLSKDLIM	EDYEVASTYPT	--TSKVRQILDITD	LOGEFKIVQKED	--NKQMGQPVPEILV
ARC	6	-EPPSETIDRERKREVELQADSG	--LLLDALVARGVLT	PEVEBALDPA	--ERRVRELLVQSKGAAC	QELLRCQOTVSP	PDAMDQWQVGP
RAIDD	1	MEERDKVIRSRERLECEVILVGG	--LVLCQLYQGHITNHI	QENAOITG	--IRKTMILLDITPSR	QPAIDFLDS	CEFPWREEMKAREEAM
Caspase-2	15	MPHROETIKQNRVILAKOLLS	--ELLELEKOLIT	PEVEBALDPA	--ERRVRELLVQSKGAAC	QELLRCQOTVSP	PDAMDQWQVGP
Ced-3	2	MODRESLEENIMFESSHKMD	--EILEVILIAQVLSN	GDMSNGTV	--EERREIVKAVORRG	VARDAFYDALRS	--TCEGAEVIEPLA
Ced-4	2	LCIECEALSTHTRLIHDFEP	--DALVILEGRNIFT	EDHSELSKMS	--EERIANFETIRYERQ	SELPIDFFEN	--NNQSHADADEFIYI
Caspase-9	1	MDADRRLRRCGRRLMELOMD	--QIMDVLSSELP	EMIEDQ	QAGSGSRDQALID	ETRGSCALPEISCH	--TGODMLASFLITNR
Apaf-1	1	MDAKRNCLQHEEALIKD	IKTS	--YIMDHMSICELTH	SEEEKVNEPTQ	--OORAAMLIKMILIK	CONDVSVSYNATH
C-IAP1	453	MASDDLSTIRKRNEMALFOOLT	CVL	--PIEDNELLKRNVIN	KOEHDIIKOKTC	--PCAREELIDIT	LVWKGNAANIFKNC

# B

Nod2	273	PATLC	-----	EEELSTPGHNDADIVLVGEAGSGKSTLLQRLHLWAAGDFOEFLVFP	-----	FSRQLOCMKAP	--LSVRTLLP	FEH	-----	CCMPDVQGEDIFQILLDHPD									
Nod1	171	NESLCSNSLACILDTITGILNEOG	ETPH	GEAGVSKMLQRLQSLWATGRLDAGKREPH	-----	EFCRMESCKESDR	LCQDLLRKH	-----	YCHERDPEWPAFLRPH										
Apaf-1	112	PVVEVTRKLVNAQOKLSKLRGEPGWTHGVAGSGKVLDAEVVDHSLLEGCPGGM	TV	--SVGKQDKSGLEMKONLCTRLDODES	SO	--RLPLANIEEKERIRLIRLHP													
Ced-4	128	MTGVIREFHVDRVKKLD	EMCDLDSFLEPHGRAGSGK	VDAESQALS	KSDQLIGVYDSH	WLDKSGTAPKSTFDLFTDILLMKS	EDDE	--ENFSPSVEHVTSVVLKRMICN	PLIDRP										
Nod2	373	RVLLTFDGEDEFKRFTRDR	--HCSPDTPSVOTLLFNLLQGNLLK	NKARVVTSP	PAASAFIRKVI	RTPEEN	--LKGFSPQGI	ELVLRKH	-----	HEPG-VADRLIRLQEB	--TS								
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Apaf-1	226	RSLLHEDDYMBS	-----	WYLKAFDS	QCOHIT	TRDKSVTD	--SYNGPKYMPV	SESSGKEKGL	ETLSLFVN	--MKKDDP	DEFOASH	ETKCKG	PLV						
Ced-4	244	NTIEVFDDYVQEE	-----	TERWAQELIR	ETVTHRDVE	SN	--AASQTG	EEFIEV	--TSEIDE	CYDDELEAYGMP	VPVGEKEE	EVNTL	ELSSGNP	--					
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Nod1	383	--NLCGLCSY	PEFCWTHFCFQ	HERAPFEGSP	OLPDCVT	ITLDMVPL	ETVTEV	LVNRC	PESS	-----	IQRNTSPMET	IRGRDTL	CSLG	-----	QMAHRCKE	SLVFT	DEBS	QAQSG	QOE
Apaf-1	313	VSEKGALEDFNRM	BEYL	-----	KOLONKOF	KRIRKSS	VDYVEND	DEANSIS	VEMLREDI	KDVT	--SILQDKWVPTKVL	CIILW	--DMTEEMED	ILQEVN	KSL	EL	CDNRG		
Ced-4	331	ATLMMFKSCPEKTEKWAQ	-----	NNKLE	ERGLVGE	CITPYS	NKSLAM	QRCYEVLS	DEDRSLAF	--VVMPPG	VDIP	VG	ECV	IPVDI	CSNEE	EQLDDE	VADRLK	KR	QEA

# C

		$\alpha$	$\beta$
Repeat 1	744	RSVEMQERERLARK	ARGNLVGHKLTF
Repeat 2	772	CSVGPTECAALAFVL	QHLRRPVALQDY
Repeat 3	800	NSVGDIGVEQLPCL	---GVCKALYERD
Repeat 4	825	NNESDRGIYKLE	CAHCEQLOKLAFFN
Repeat 5	853	NKQTDGCAHSM	AKILLACRQNHALLRGN
Repeat 6	881	NYVTAAQAQVLA	EGLRGNTSLOFTGANG
Repeat 7	909	NNQDGEQAQAL	AEALGDHQSRLWLSVG
Repeat 8	937	NNQSVGAQAL	ALMLAKNMVLEELCEE
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Repeat 10	993	NCEVYLGA	REALQALERNDTLEVMERG

Figure 2



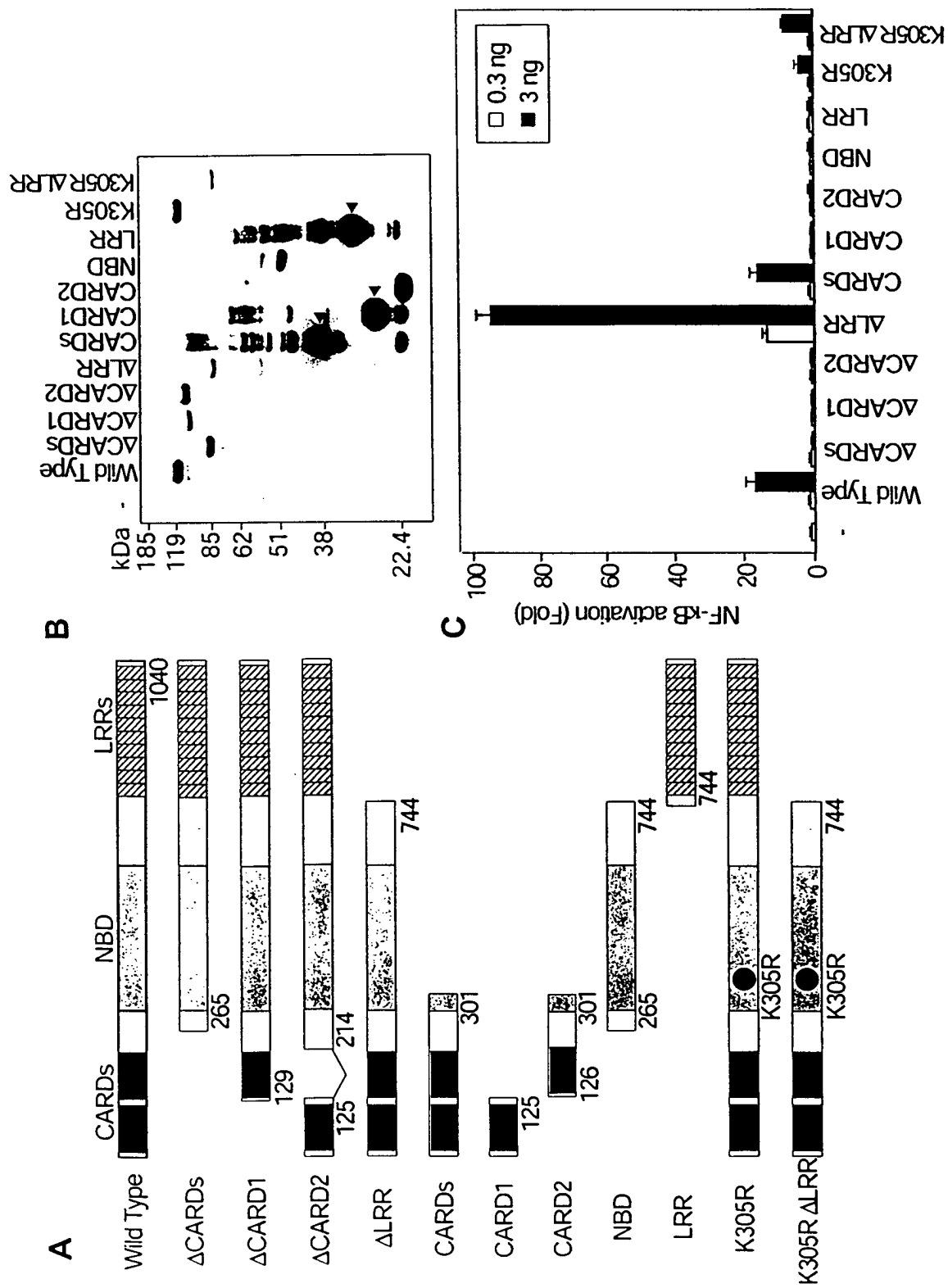


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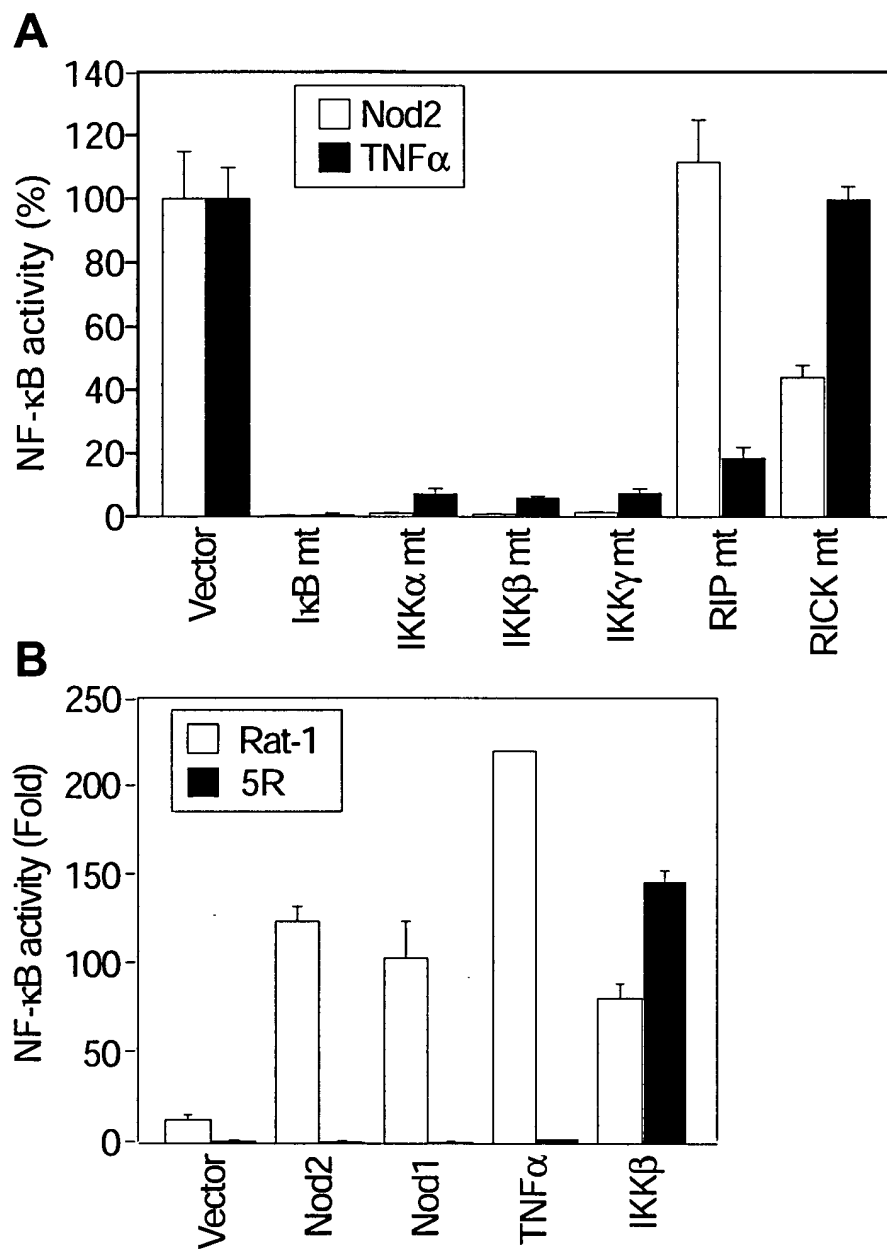


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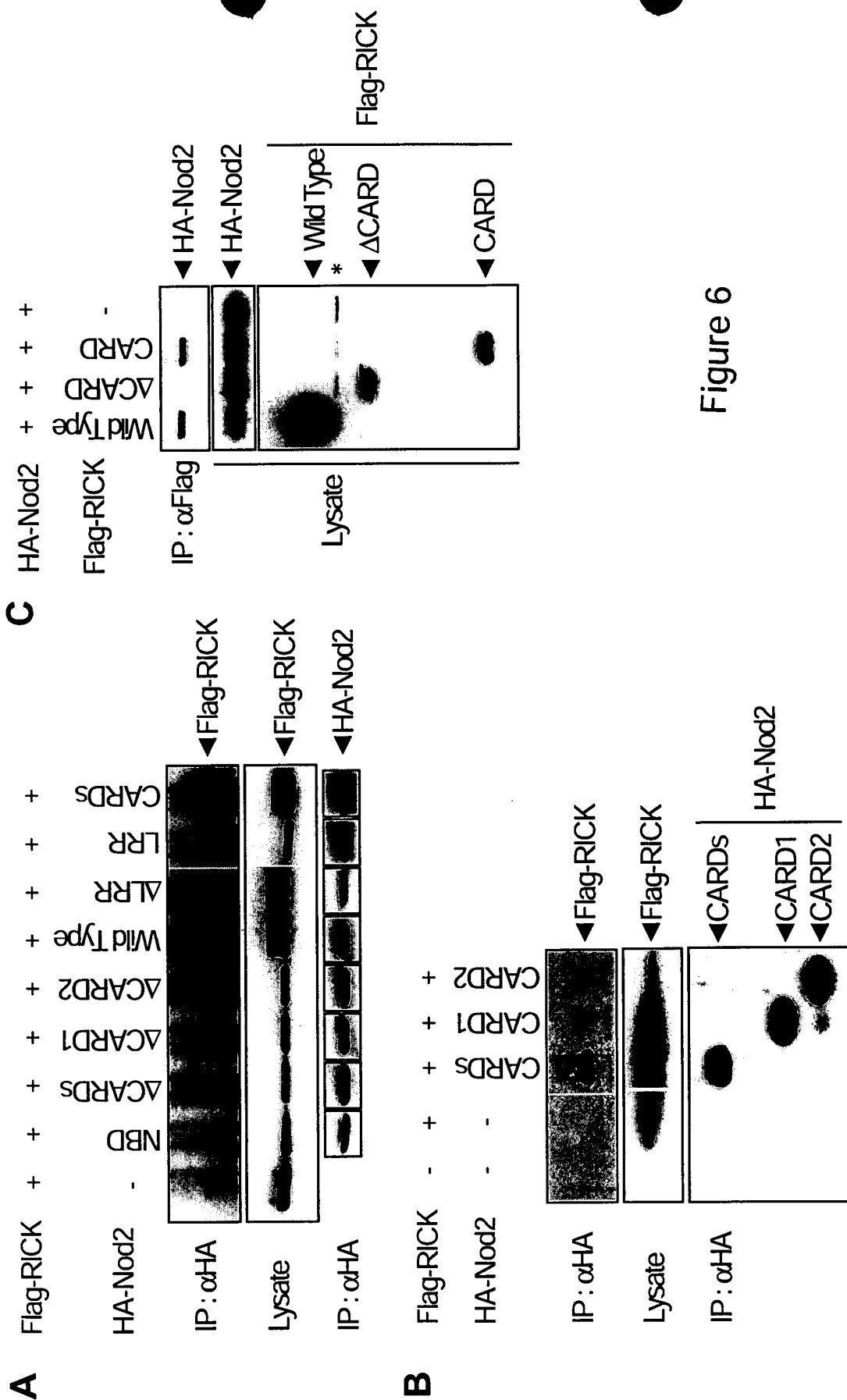


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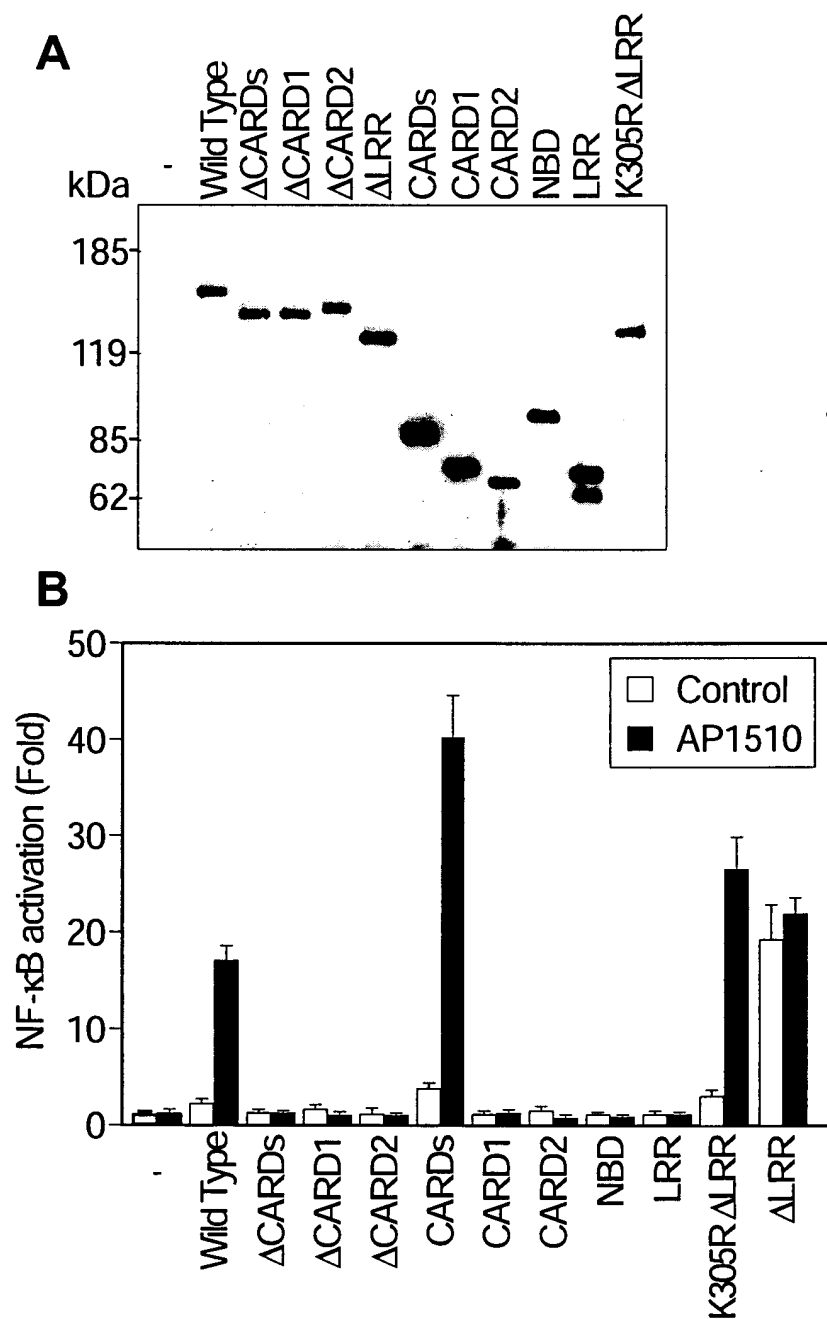
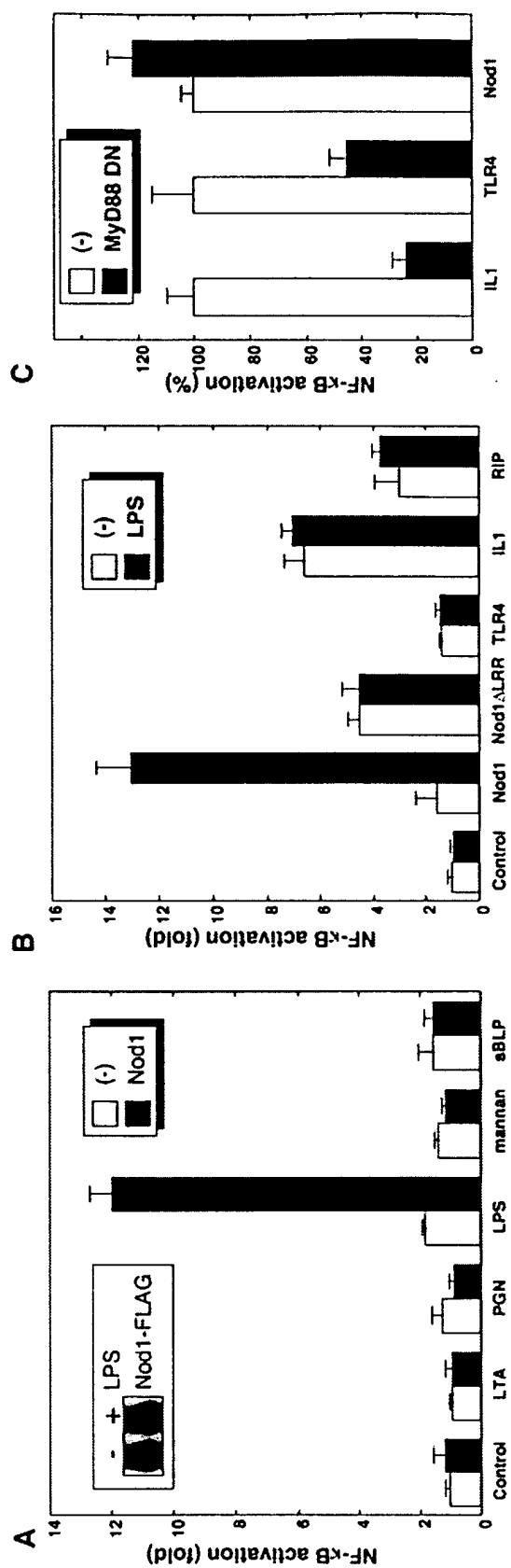


Figure 7



**Figure 8**



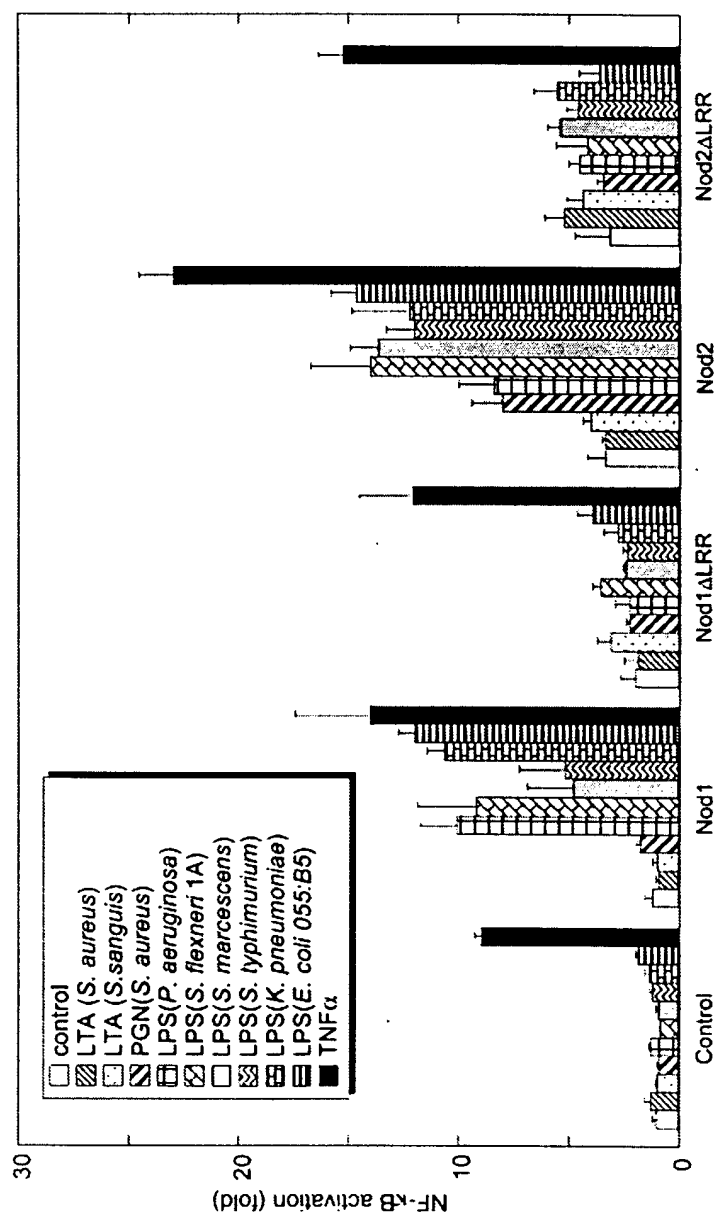


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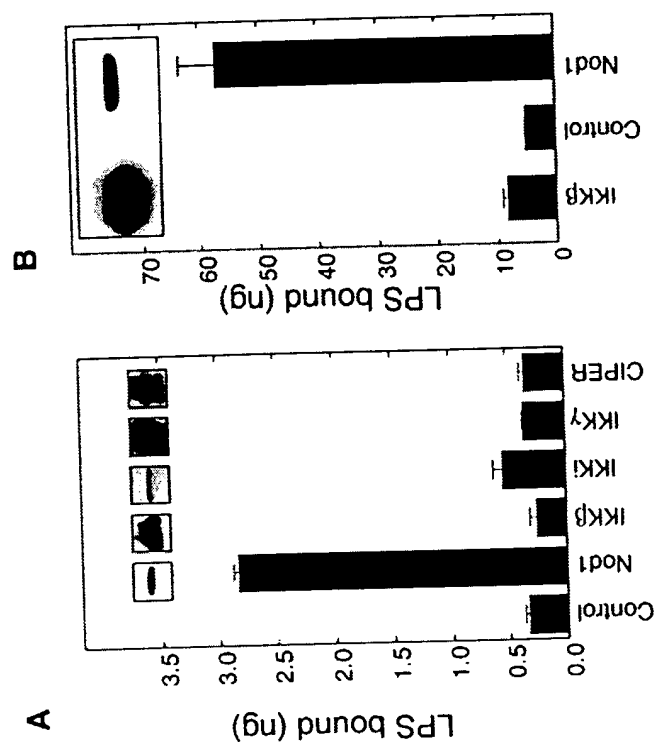


Figure 10

## Figure 11

### SEQ ID NO:33

#### Nod2 cDNA sequence

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**SEQ ID NO:1**

### Nod2 cDNA sequence

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人口	12,000	12,500	13,000	13,500	14,000	14,500	15,000	15,500	16,000	16,500	17,000	17,500	18,000	18,500	19,000	19,500	20,000	20,500	21,000	21,500	22,000	22,500	23,000	23,500	24,000	24,500	25,000	25,500	26,000	26,500	27,000	27,500	28,000	28,500	29,000	29,500	30,000	30,500	31,000	31,500	32,000	32,500	33,000	33,500	34,000	34,500	35,000	35,500	36,000	36,500	37,000	37,500	38,000	38,500	39,000	39,500	40,000	40,500	41,000	41,500	42,000	42,500	43,000	43,500	44,000	44,500	45,000	45,500	46,000	46,500	47,000	47,500	48,000	48,500	49,000	49,500	50,000	50,500	51,000	51,500	52,000	52,500	53,000	53,500	54,000	54,500	55,000	55,500	56,000	56,500	57,000	57,500	58,000	58,500	59,000	59,500	60,000	60,500	61,000	61,500	62,000	62,500	63,000	63,500	64,000	64,500	65,000	65,500	66,000	66,500	67,000	67,500	68,000	68,500	69,000	69,500	70,000	70,500	71,000	71,500	72,000	72,500	73,000	73,500	74,000	74,500	75,000	75,500	76,000	76,500	77,000	77,500	78,000	78,500	79,000	79,500	80,000	80,500	81,000	81,500	82,000	82,500	83,000	83,500	84,000	84,500	85,000	85,500	86,000	86,500	87,000	87,500	88,000	88,500	89,000	89,500	90,000	90,500	91,000	91,500	92,000	92,500	93,000	93,500	94,000	94,500	95,000	95,500	96,000	96,500	97,000	97,500	98,000	98,500	99,000	99,500	100,000

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10002974 102604

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gatgctgtgc aaatgttatt attttaaaca ttatgatgtg tgaaaactgg ttaatattta	4380
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Figure 13  
SEQ ID NO:2

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GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTPSQR  
ARRLLDLATV KANGLAAFLQ QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY  
DGAETLCLED IYTENVLEW ADVGMAGPPQ KSPATLGLLE LFSTPGHLND DADTVLVVGE  
AGSGKSTLLQ RLHLLWAAGQ DFQEFLLVFP FSCRQLQCMA KPLSVRTLLF EHCCWPDVGO  
EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLFNL LQGNLLKNAR  
KVVTSRPAAV SAFLRKYIRT EFNKLGFEQ GIELYLRKRH HEPGVADRLI RLLQETSALH  
GLCHLPVFSW MVSCKHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL  
RGRLPTLLHL GRLALWGLGM CCYVFAQQL QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE  
FLHITFQCFE AAFYLALSAD VPPALLRHLE NCGRPGNSPM ARLLPTMCIQ ASEGKDSSVA  
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH  
SIPPAAPGEA KSVHAMPGEI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTCA  
ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL  
HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQV LAEGLRGNTS  
LQFLGFWGNR VGDEGAQALA EALGDHQSLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL  
CLEENHLQDE GVCSLAELK KNSSLKILKL SNNCITYLGA EALLQALERN DTILEVWLRG  
NTFSLEEVDK LGCRDTRLLL \*

10002974-102601

## Figure 14

SEQ ID NO:3

MCSQEAFQAA RSQVLELLVS GSLEGFESVL DWLLSWEVLS WEDYEGFHLL GQPLSHLARR  
LLDTVWNKGT WACQKLIAAA QEAQADSQSP KLHGCWDPHS LHPARDLQSH RPAIVRRLLHS  
HVENMLDLAW ERGFVSQYEC DEIRLPIFTP SQRARRLLDL ATVKANGLAA FLLQHVQELP  
VPLALPLEAA TCKKYMALR TTVSAQSRFL STYDGAETLC LEDIYTENVL EVWADVGMAG  
PPQKSPATLG LEELFSTPGH LNDDADTVLV VGEAGSGKST LLQRLHLLWA AGQDFQEFLF  
VFPFSCRQLQ CMAKPLSVRT LLFEHCCWPD VGQEDIFQLL LDHPDRVLLT FDGFDEFKFR  
FTDRERHCSP TDPTSVQTLL FNLLQGNLLK NARKVVTSRP AAVSAFLRKY IRTEFNLKGF  
SEQGIELYLR KRHHEPGVAD RLIRLLQETS ALHGLCHLPV FSWMVSKCHQ ELLQEGGSP  
KTTTDMYLLI LQHFLHATP PDSASQGLGP SLLRGRLPTL LHLGRLALWG LGMCCYVFA  
QQLQAAQVSP DDISLGFLVR AKGVVPGSTA PLEFLHITFQ CFFAAFYAL SADVPPALLR  
HLFNCGRPGN SPMARLLPTM CIQASEGKDS SVAALLQKAE PHNLQITAAF LAGLLSREHW  
GLLAECQTSE KALLRRQACA RWCLARSLRK HFHSIPPAAP GEAKSVHAMP GFIWLIRSLY  
EMQEERLARK AARGLNVGHL KLTFCVSGPT ECAALAFVLQ HLRRPVALQL DYNSVGDIGV  
EQLLPCLGVC KALYLRDNNI SDRGICKLIE CALHCEQLQK LALFNNKLTG GCAHSMAKLL  
ACRQNFLALR LGNNYITAAG AQVLAEGLRG NTSLQFLGFW GNRVGDEGAQ ALAEALGDHQ  
SLRWLSLVGN NIGSVGAQAL ALMLAKNVML EELCLEENHL QDEGVCSLAE GLKKNSSLKI  
LKLSNNCITY LGAEALLQAL ERNDTILEVW LRGNTFSLEE VDKLGCRDTR LLL\*

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Figure 15  
SEQ ID NO:34

Nod2a AA sequence, Mutant

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GCWDPHSLHP ARDLQSHRPA IVRRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTSPQR  
ARRLLDLATV KANGLAAFL LQHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY  
DGAETLCLED IYTENVLEVW ADVGMAGPPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE  
AGSGKSTLLQ RLHLLWAAGQ DFQEFLFVFP FSCRQLQCM KPLSVRTLLF EHCCWPDVGO  
EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLEFN LQGNLLKNAR  
KVVTSRPAAV SAFLRKYIRT EFNKGFSEQ GIELYLRKRH HEPGVADRLL RLLQETSALH  
GLCHLPVFSW MVSKCHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL  
RGRLPTLLHL GRLALWGLGM CCYVFAQQ LQAAQVSPDDI SLGFLVRAKG VVPGSTAPLE  
FLHITFQCFE AAFYLALSAD VPPALLRHLE NCGRPGNSPM ARLLPTMCIQ ASEKGDSSVA  
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH  
SIPPAAPGEA KSVHAMPFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTECA  
ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL  
HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGA QV LAEGLRGNTS  
LQFLGFWGNR VGDEGAQALA EALGDHQLSR WLSLVGNNIG SVGAQALALM LAKNVMLEEL  
CLEENHLQDE GVCSLAELK KNSSLKILKL SNNCITYLGA EALLQAP\*

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## FIGURE 16

### Nod2 Exon11, Wild type

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cagtctcttt aactggacag tttcaagagg aaaaccaaga atccttgaag ctcaccattg

tatcttcttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT GAAAGGAATG ACACCATCCT GGAAGTCTGg taaggcccct gggcaggcct

Q A L E R N D T I L E V

gttttagctc tccgaacctc agtttttcta tctgtaaaat ggggtgacgg gagagaggaa

tggcagaatt ttgaggatcc cttctgattc tgacattcag tgagaatgat tctgcatgtg

### Nod2 Exon11, Mutant

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cagtctcttt aactggacag tttcaagagg aaaaccaaga atccttgaag ctcaccattg

tatcttcttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT TGAAAGGAAT GACACCATCC TGGAAGTCTG gtaaggcccc tgggcaggcc

Q A P \*

tgtttttagct ctccgaacct cagtttttct atctgtaaaa tggggtgacg ggagagagga

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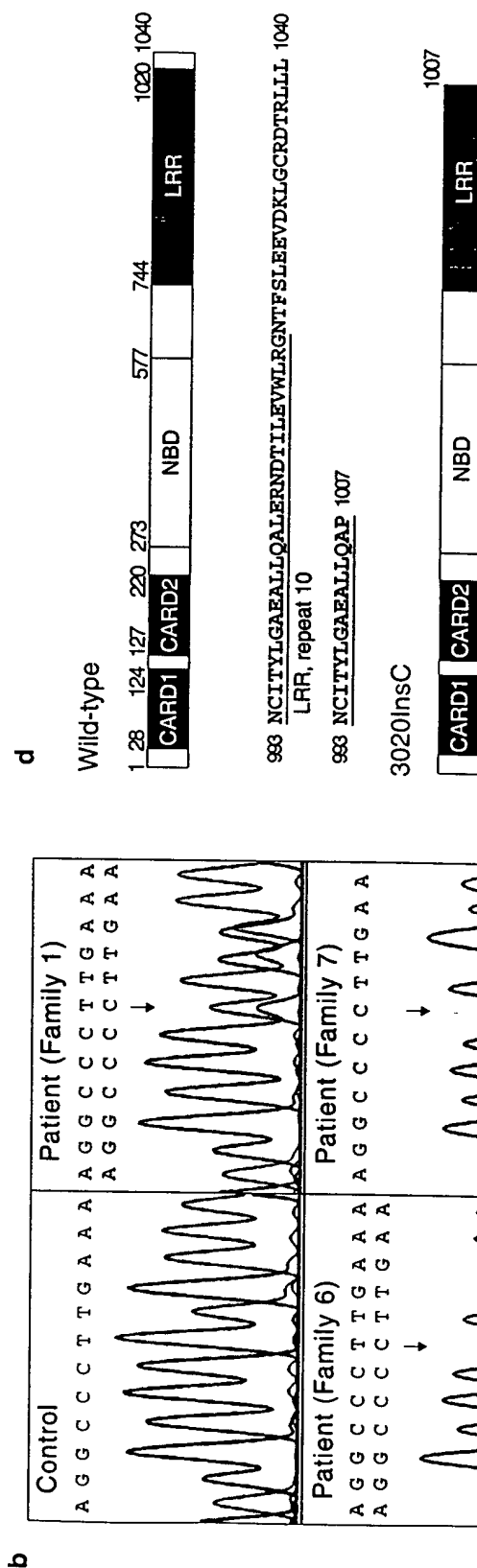
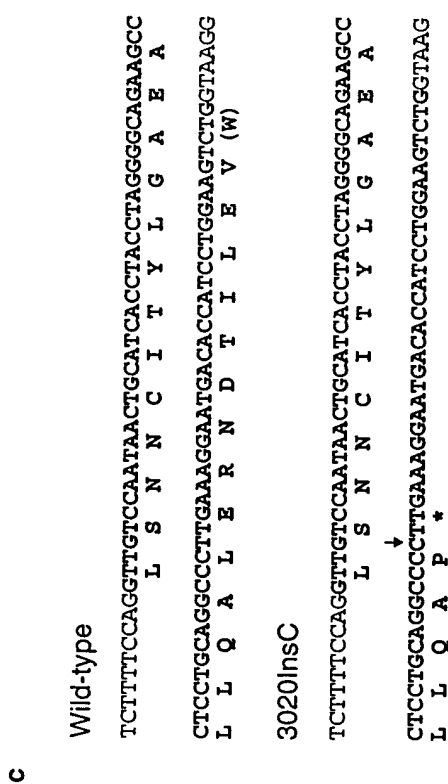
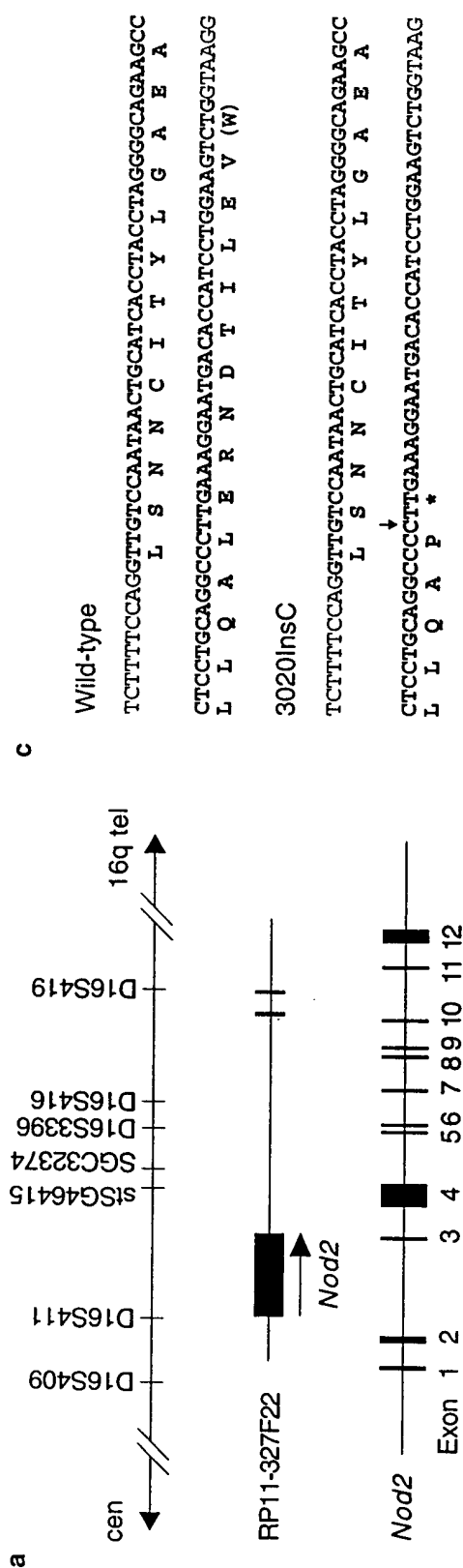


Figure 17

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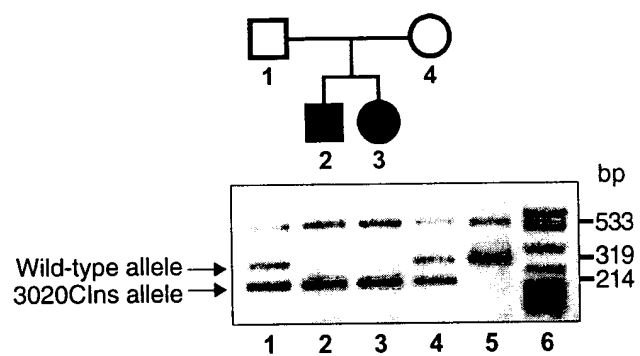


Figure 18

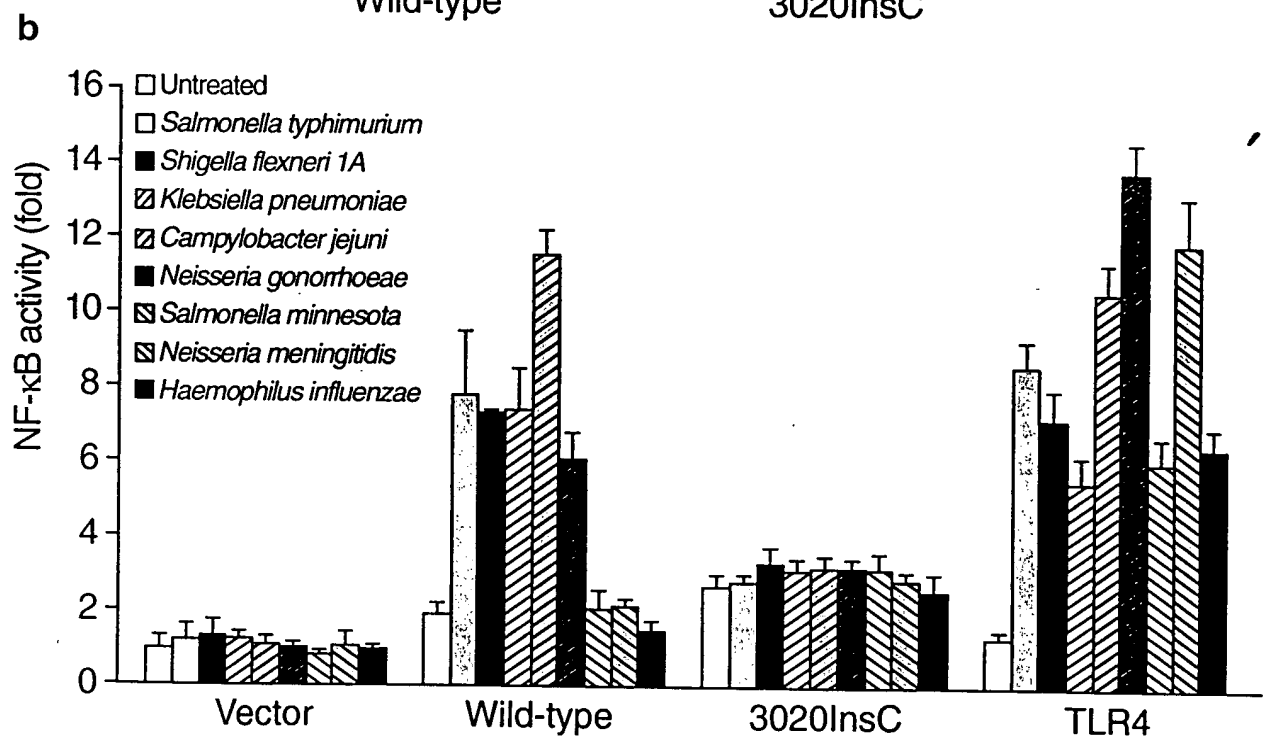
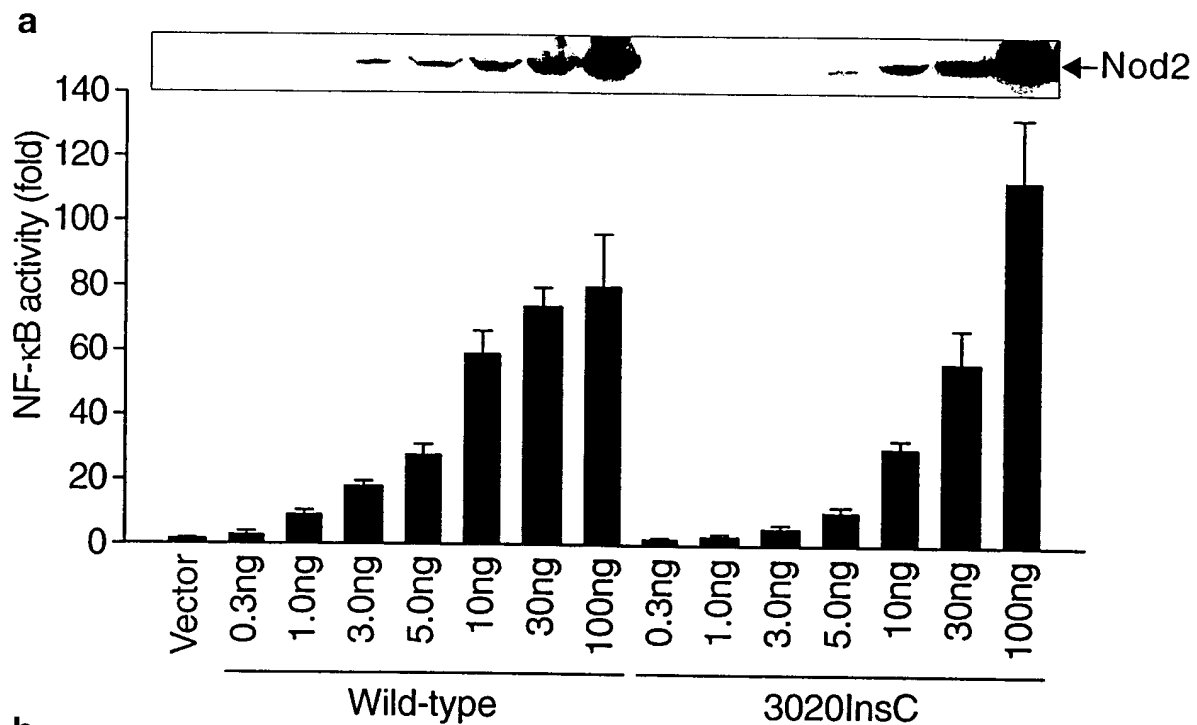


Figure 19



Figure 20  
SEQ ID NO: 53

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Figure 21  
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10002974-102601

# Figure 22

## SEQ ID NO: 55

60 MGEEGGSASH DEERASVLL GHSPGCEMCS QEAFQAQRSQ LVELLVSGSL EGFESVLDWL  
 120 LSWEVLSWED YEGFHLLGQP LSHLARLLD TVWNKGTWAC QKLIAAAQEA QADSQSPKLH  
 180 GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTPSQR  
 240 ARRLDLATV KANGLAFL L QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY  
 300 DGAETLCLED IYTENVLEVW ADVGMAGSPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE  
 360 AGSGKSTLLQ RLHLLWAAGQ DFQEFLLVFP FSCRQLQCMA KPLSVRTLFL EHCCWPDVGQ  
 420 EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLEFN LQGNLLKNAR  
 480 KVVTSRPAAV SAFLRKYIRT EFNKGFSEQ GIELYLRKRH HEPGVADRLI RLLQETSALH  
 540 GLCHLPVFSW MVSCHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL  
 600 RGRLPTLLHL GRLALWGLM CCYVFSQQ L QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE  
 660 FLHITFQCFF AAFYLALSAD VPPALLRHLF NCGRPGNSPM ARLLPTMCIQ ASEKGDSSVA  
 720 ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH  
 780 SIPPAAPGEA KSVHAMPFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTECA  
 840 ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL  
 900 HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGA QV LAEGLRGNTS  
 960 LQFLGFWG NR VGDEGAQALA EALGDHQLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL  
 1007 CLEENHLQDE GVCSLAEG LK KNSSLKILKL SNNCITYLGA EALLQAP\*

10002974.102601

Figure 23  
SEQ ID NO: 56

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tga

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**Figure 24**  
**SEQ ID NO: 57**

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQVLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
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FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLLVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPTLLHLGRLALWGLGM  
CCYVFSAAQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLWRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTCAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFALRLGN  
NYITAAGAQLVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQLRWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL

\*

100022974.10260.1

Figure 25  
SEQ ID NO: 58

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tga

10002974.102604

SNP	Allele	SNP Sequence*	AA Polymorphism	AA Location	cDNA Location
SNP4	1	GGCAGATGTGGGCATGGCTGGACCC; SEQ ID NO:70	P	P 268 S	nt 802
	2	GGCAGATGTGGGCATGGCTGGAICC; SEQ ID NO:71	S		
SNP20	1	AGACATCTGAGAAGGCCCTGCTCCGG; SEQ ID NO:72	R	R 702 W	nt 2104
	2	AGACATCTGAGAAGGCCCTGCTCTGG; Seq ID NO:73	W		
SNP7	1	CTGCAGCACCTCCGGCGGCCCGTGG; SEQ ID NO:74	V	V 793 M	nt 2377
	2	CTGCAGCACCTCCGGCGGCCCATG; SEQ ID NO:75	M		
SNP18	1	TTGCAGAAGTTAGCTCTATTCAAC; SEQ ID NO:76	N	N 852 S	nt 2555
	2	TTGCAGAAGTTAGCTCTATTGAGC; SEQ ID NO:77	S		
SNP25	1	ACTGACGGCTGTGCACACTCCATG; SEQ ID NO:78	M	M 863 V	nt 2587
	2	ACTGACGGCTGTGCACACTCCGTG; SEQ ID NO:79	V		
SNP17	1	TGCAGTTCCTGGGATTCTGGGGC; SEQ ID NO:80	G	G 908 R	nt 2722
	2	TGCAGTTCCTGGGATTCTGGCGC; SEQ ID NO:81	R		
SNP23	1	CACTGATGCTGGCAAAGAACGTC; SEQ ID NO:82	V	V 955 I	nt 2863
	2	CACTGATGCTGGCAAAGAACATC; SEQ ID NO:83	I		
3020C Ins	1	GGGCAGAAAGCCCCTCCTGCAGGCCCT; SEQ ID NO:90	wild-type		nt 3020
	2	GGGCAGAAAGCCCCTCCTGCAGGCCCT; SEQ ID NO:91	frameshift mutation	Δ33	
		*Underlined is mutated base			
		*Nucleotide/amino acid numbers designate the positions in Nod2a as reported by Ogura et al. J. Biol. Chem. 276:4812 [2001]			
		AA = amino acid			
		SNP= single nucleotide polymorphism			

Figure 26





Figure 28  
SEQ ID NO: 59

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLGQP  
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FVSQYECDEIRLPIFTPSQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLLPTLLHLGRLLALWGLGM  
CCYVFSAAQQLQAAQVSPDDISLGFLVRAGVVPGSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIIRSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTCAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMKLLACRQNFALRLGN  
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\*

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Figure 29  
SEQ ID NO: 60

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10002974.102601

Figure 30  
SEQ ID NO: 61

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10002974.102601

Figure 31  
SEQ ID NO: 62

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10002974.102601

Figure 32  
SEQ ID NO: 63

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10002974-102604

Figure 33  
SEQ ID NO: 64

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10002974-102601

Figure 34  
SEQ ID NO: 65

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\*

10002974-102601

Figure 35  
SEQ ID NO: 66

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tga

10002974.102601



Figure 36  
SEQ ID NO: 67

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
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FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRILIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLEPTLLHLGRLALWGLGM  
CCYVFSAAQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCSSVGPTCAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMKLLACRQNFALRLGN  
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNIMLEEL  
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL  
\*

10002974.102601

Figure 37  
SEQ ID NO: 68

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tga

10002974-102601

Figure 38  
SEQ ID NO: 69

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
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FVSQYECDEIRLPIFTPSQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRILIRLLQETSALH  
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRPLTLLHLGRLLALWGLM  
CCYVFSAAQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTCAALAFVLQHLRRPVALQLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSVAKLLACRQNFALRLGN  
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQLRWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
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\*

10002974-102604

Figure 39  
SEQ ID NO: 84

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tga

10002974-100001

Figure 40  
SEQ ID NO: 85

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQVLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
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FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQLQHVQELPVPLALPLEAATCKKYMALRRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHHEPGVADRILIRLLQETSALH  
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CCYVFSQQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM  
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH  
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCVSGPTECAALAFVLQHLRRPVALQOLDYN  
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNKLTDGCAHSMKLLACRQNFALRLGN  
NYITAAGAVLAEGLRGNTSLQFLGFWRNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNVMLEEL  
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\*

10002974-102604

Figure 41  
SEQ ID NO: 86

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tga

10002974.102601

Figure 42  
SEQ ID NO: 87

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP  
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FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRRTTVSAQSRFLSTY  
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ  
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP  
TSVQTLLENLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRILIRLLQETSALH  
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SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFSNKLTDGCAHSMALLACRQNFALRLGN  
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\*

1002974.102601

Figure 43  
SEQ ID NO: 88

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Figure 44  
SEQ ID NO: 89

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